

Figure 4A: Aligned hedg-5 cDNA and predicted amino acid sequence. The first 250 bp of DNA sequence (lower case) is derived from genomic DNA flanking the 5' end of the cDNA insert from clone pC3-hedg5-3. Sequences from nt 251-1523 are shown in lower case wherever apparent polymorphisms in different human clones were found. Coding region polymorphisms are detailed in Table 1. One intron exists within the coding region of hedg-5, located between nt 996/997 of the cDNA sequence shown.

1 cacccttcctaacctgagcggcctagcctgggaaacaaacaattaaaatgtgcgctaaatg 60  
-----+-----+-----+-----+-----+-----+-----+  
gtggaaggattggactcgccggatcggaacctttgtttgttaattttacacgcgatttac  
61 ctgtggtaggaggtcaggggctatgtcctggaccaaaggacatttgcactgagacctgac 120  
-----+-----+-----+-----+-----+-----+-----+  
gacaccatcctccagtcctccgatacaggacctggtttcctgtaaacgtgactctggactg  
121 acttcaggtcttcaactcccttgatgggagttagccagaacgggcttagaaacagcaatt 180  
-----+-----+-----+-----+-----+-----+-----+  
tgaagtccagaagttgaggggaactaccctcaatcggtcttgcccgaatctttgtcgttaa  
181 gatggcttagtgactgattttacaaatgatatttgtttcttctttaatttctttctagg 240  
-----+-----+-----+-----+-----+-----+-----+  
ctaccgaatcactgactaaaatgtttactataaacaagaagaatttaaagaagatcc  
M N E C H Y D K H M D F F Y  
241 atgttcacttCTTCTCCACAATGAATGAGTGTCACTATGACAAGCACATGGACTTTTTTT 300  
-----+-----+-----+-----+-----+-----+-----+  
tacaagtgaagaagAGGTGTTACTTACTCACAGTGATACTGTTCTGTGTACCTGAAAAAAA  
N R S N T D T V D D W T G T K L V I V L  
301 ATAATAGGAGCAACACTGATACTGTGCTGACTGGACAGGAACAAAGCTTGTGATTGTTT 360  
-----+-----+-----+-----+-----+-----+-----+  
TATTATCCTCGTTGTGACTATGACAGCTACTGACCTGTCCTTGTTTCGAACACTAACAA  
C V G T F F C L F I F F S N S L V I A A  
361 TGTGTGTTGGGACGTTTTCTGCCTGTTTATTTTTTTTTTCTAATTCTCTGGTCATCGCGG 420  
-----+-----+-----+-----+-----+-----+-----+  
ACACACAACCCTGCAAAAAGACGGACAAATAAAAAAAGATTAAGAGACCAGTAGCGCC  
V I K N R K F H F P F Y Y L L A N L A A  
421 CAGTGATCAAAAACAGAAAATTTCAATTTCCCTTTTACTACCTGTTGGCTAATTTAGCTG 480  
-----+-----+-----+-----+-----+-----+-----+  
GTCAGTAGTTTTTGTCTTTTAAAGTAAAGGGGAAATGATGGACAACCGATTAAATCGAC  
A D F F A G I A Y V F L M F N T G P V S  
481 CTGCCGATTTCTTCGCTGGAATTGCCTATGTATTCCTGATGTTTAACACAGGCCAGTTT 540  
-----+-----+-----+-----+-----+-----+-----+  
GACGGCTAAAGAAGCGACCTTAACGGATACATAAGGACTACAAATTGTGTCCGGGTCAAA  
K T L T V N R W F L R Q G L L D S S L T  
541 CAAAACTTTGACTGTCAACCGCTGGTTTCTCCGTCAGGGGCTTCTGGACAGTAGCTTGA 600  
-----+-----+-----+-----+-----+-----+-----+  
GTTTTTGAACTGACAGTTGGCGACCAAAGAGGCAGTCCCCGAAGACCTGTCATCGAACT

Figure 4A (cont.)



601 A S L T N L L V I A V E R H M S I M R M  
CTGCTTCCCTCACCAACTTGCTGGTTATCGCCGTGGAGAGGCACATGTCAATCATGAGGA  
-----+-----+-----+-----+-----+ 660  
GACGAAGGGAGTGGTTGAACGACCAATAGCGGCACCTCTCCGTGTACAGTTAGTACTCCT  
R V H S N L T K K R V T L L I L L V W A  
661 TGCGGGTCCATAGCAACCTGACCAAAAAGAGGGTGACACTGCTCATTTTGCTTGTCTGGG  
-----+-----+-----+-----+-----+ 720  
ACGCCAGGTATCGTTGGACTGGTTTTTCTCCACTGTGACGAGTAAACGAACAGACCC  
I A I F M G A V P T L G W N C L C N I S  
721 CCATCGCCATTTTATGGGGGCGGTCCCCACACTGGGCTGGAATTGCCTCTGCAACATCT  
-----+-----+-----+-----+-----+ 780  
GGTAGCGGTAAAAATACCCCCGCCAGGGGTGTGACCCGACCTTAACGGAGACGTTGTAGA  
A C S S L A P I Y S R S Y L V F W T V S  
781 CTGCTGCTCTTCCCTGGCCCCCATTTACAGCAGGAGTTACCTTGTTTTCTGGACAGTGT  
-----+-----+-----+-----+-----+ 840  
GACGGACGAGAAGGGACCGGGGTAAATGTCGTCCTCAATGGAACAAAAGACCTGTCACA  
N L M A F L I M V V V Y L R I Y V Y V K  
841 CCAACCTCATGGCCTTCTCATCATGTTGTGGTGTACCTGCGGATCTACGTGTACGTCA  
-----+-----+-----+-----+-----+ 900  
GGTTGGAGTACCGGAAGGAGTAGTACCAACACCACATGGACGCCTAGATGCACATGCAGT  
R K T N V L S P H T S G S I S R R R T P  
901 AGAGGAAAACCAACGTCTTGTCTCCGCATACAAGTGGGTCCATCAGCCGCCGGAGGACAC  
-----+-----+-----+-----+-----+ 960  
TCTCCTTTTGGTTGCAGAACAGAGGCGTATGTTACCCAGGTAGTCGGCGGCCTCCTGTG  
M K L M K T V M T V L G A F V V C W T P  
961 CCATGAAGCTAATGAAGACGGTGATGACTGTCTTAGGGGCGTTTGTGGTATGCTGGACCC  
-----+-----+-----+-----+-----+ 1020  
GGTACTTCGATTACTTCTGCCACTACTGACAGAATCCCCGAAACACCATACGACCTGGG  
G L V V L P L D G L N C R Q C G V Q H V  
1021 CGGGCCTGGTGGTTCTGCCCCCTCGACGGCCTGAACTGCAGGCAGTGTGGCGTGCAGCATG  
-----+-----+-----+-----+-----+ 1080  
GCCCCGACCACCAAGACGGGGAGCTGCCGACTTGACGTCCGTACACCCGCACGTCGTAC  
K R W F L L L A L L N S V V N P I I Y S  
1081 TGAAAAGGTGGTTCTGCTGCTGGCGCTGCTCAACTCCGTCTGTAACCCCATCATCTACT  
-----+-----+-----+-----+-----+ 1140  
ACTTTTCCACCAAGGACGACGACCGCGACGAGTTGAGGCAGCACTTGGGGTAGTAGATGA  
Y K D E D M Y G T M K K M I C C F S Q E  
1141 CCTACAAGGACGAGGACATGTATGGCACCATGAAGAAGATGATCTGCTGCTTCTCTCAGG  
-----+-----+-----+-----+-----+ 1200  
GGATGTTCTGCTCCTGTACATACCGTGGTACTTCTTCTACTAGACGACGAAGAGAGTCC  
N P E R R P S R I P S T V L S R S D T G  
1201 AGAACCCAGAGAGGCGTCCCTCTCGCATCCCCCTCCACAGTCTCAGCAGGAGTGACACAG  
-----+-----+-----+-----+-----+ 1260  
TCTTGGGTCTCTCCGCAGGGAGAGCGTAGGGGAGGTGTGAGGAGTCGTCCTCACTGTGTC  
S Q Y I E D S I S Q G A V C N K S T S \*  
1261 GCAGCCAGTACATAGAGGATAGTATTAGCCAAGGTGCAGTCTGCAATAAAAGCACTTCCT  
-----+-----+-----+-----+-----+ 1320  
CGTCGGTCATGTATCTCCTATCATAATCGGTTCCACGTGACGCGTTATTTTCGTGAAGGA

Figure 4A (cont.)

AAACTCTGGATGCCTCTYGGCCACCCAGGCCTCCTCTGGGAAAAGAGCTGTTAAGAATG  
1321 -----+-----+-----+-----+-----+-----+-----+ 1380  
TTTGAGACCTACGGAGARCCGGTGGGTCCGGAGGAGACCCTTTTCTCGACAATTCTTAC  
ATTACCTGTCTCTAACAAGCCCATGTACAGTGTTATTTGAGGTCTCCATTAATCACTGC  
1381 -----+-----+-----+-----+-----+-----+-----+ 1440  
TAATGGACAGAGATTGTTTCGGGTACATGTACAATAAACTCCAGAGGTAATTAGTGACG  
TAGATTTCTTTAAAAAATTTTTTTTCATAGTTTAAAAGCATGGGCAGTAAAGAGAGGACC  
1441 -----+-----+-----+-----+-----+-----+-----+ 1500  
ATCTAAAGAAATTTTTTAAAAAAAAGTATCAAATTTTCGTACCCGTCATTCTCTCTCGG  
TGCTGCATTTAGAGAAAGCACAG  
1501 -----+-----+-----+-----+-----+-----+-----+ 1523  
ACGACGTAAATCTCTTTTCGTGTC

Figure 4B: Predicted amino acid sequence of hEDG5 encoded by clone pC3-hEDG5#3.4

1 MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFE CLFIFFSNL  
51 VIAAVIKNRK FHFPFYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN  
101 RWFLRQGLLD SSLTASLTNL LVIAVERHMS IMRMRVHSNL TKKRVTLILL  
151 LVWAIAIFMG AVPTLGWNCL CNISACSSLA PIYSRSYLVF WTVSNLMAFL  
201 IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT VMTVLGAFVV  
251 CWTPLGLVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVNP IIYSYKDEDM  
301 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK  
351 STS

Figure 4C: Predicted amino acid sequence of hEDG5 encoded by clone pC3-hEDG5#28.

1 MNECHYDKHM DFFYNRGNTD TVDDWTGTLK VIVLCVGTFE CLFIFFSNL  
51 VIAAVIKNRK FHFPFYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN  
101 RWFLRQGLLD SSLTASLTNL LVIAVERHMS IMRMRVHSNL TKKRVTLILL  
151 LVWAIAIFMG AVPTLGWNCL CNISACSSLA PIYSRSYLVF WTVSNLMAFL  
201 IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT VMTVLGAFVV  
251 CWTPLGLVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVNP IIYSYKDEDM  
301 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK  
351 STS

pC3-hedg55 has been  
replaced.



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      caccttcctaacctgagcgccctagcctgggaaacaaacaattaaaatgtgcgctaaatg
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
      gtggaaggattggactcgccgatcgacccttggttgttaattttacacgcgatttac
      ctgtggtaggaggtcaggggctatgtcctggaccaaaggacatttgcactgagacctgac
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
      gacaccatcctccagtcctccgatacaggacctggtttcctgtaaactgactctggactg
      acttcaggtcttcaagtcccttgatgggagttagccagaacgggcttagaaacagcaatt
121  -----+-----+-----+-----+-----+-----+-----+-----+ 180
      tgaagtcacagaagttgaggggaactaccctcaatcggctcttgcccgaatctttgtcgtaa
      gatggcttagtgactgattttacaaatgatatttgtttcttctttaatttctttctagg
181  -----+-----+-----+-----+-----+-----+-----+-----+ 240
      ctaccgaatcactgactaaaaatgtttactataaacaagaagaatttaagaaagatcc
      M N E C H Y D K H M D F F Y
      atgttcacttCTTCTCCACAATGAATGAGTGTCACTATGACAAGCACATGGACTTTTTTT
241  -----+-----+-----+-----+-----+-----+-----+-----+ 300
      tacaagtgaagaagAGGTGTTACTTACTCACAGTGATACTGTTTCGTGTACCTGAAAAAAA
      N R S N T D T V D D W T G T K L V I V L
      ATAATAGGAGCAACACTGATACTGTGATGACTGGACAGGAACAAAGCTTGTGATTGTTT
301  -----+-----+-----+-----+-----+-----+-----+-----+ 360
      TATTATCCTCGTTGTGACTATGACAGCTACTGACCTGTCCTTGTTCGAACACTAACAAA
      C V G T F F C L F I F F S N S L V I A A
      TGTGTGTTGGGACGTTTTTCTGCCTGTTTATTTTTTTTTTCTAATTCTCTGGTCATCGCGG
361  -----+-----+-----+-----+-----+-----+-----+-----+ 420
      ACACACAACCCTGCAAAAAGACGGACAAATAAAAAAAGATTAAGAGACCAGTAGCGCC
      V I K N R K F H F P F Y Y L L A N L A A
      CAGTGATCAAAAACAGAAAATTTTCAATTTCCCTTTTACTACCTGTTGGCTAATTTAGCTG
421  -----+-----+-----+-----+-----+-----+-----+-----+ 480
      GTCAGTAGTTTTTGTCTTTTAAAGTAAAGGGGAAAATGATGGACAACCGATTAAATCGAC
      A D F F A G I A Y V F L M F N T G P V S
      CTGCCGATTTCTTCGCTGGAATTGCCTATGTATTCTGATGTTTAACACAGGCCAGTTT
481  -----+-----+-----+-----+-----+-----+-----+-----+ 540
      GACGGCTAAAGAAGCGACCTTAACGGATACATAAGGACTACAAATTGTGTCCGGGTCAAA
      K T L T V N R W F L R Q G L L D S S L T
      CAAAACTTTGACTGTCAACCGCTGGTTTCTCCGTCAGGGGCTTCTGGACAGTAGCTTGA
541  -----+-----+-----+-----+-----+-----+-----+-----+ 600
      GTTTTTGAACTGACAGTTGGCGACCAAGAGGCAGTCCCCGAAGACCTGTCATCGAACT

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